

RAW SEQUENCE LISTING

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Application Serial Number: 10/524,295
Source: PCT
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PATENT APPLICATION: US/10/524,295

DATE: 01/24/2006

TIME: 10:24:58

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J524295.raw

5 <110> APPLICANT: TransMIT Gesellschaft for Technologietransfer mbH
 7 TransMIT Gesellschaft for Technologietransfer mbH
 11 <120> TITLE OF INVENTION: Method for screening the allelic state at the 5'-flanking
 region of the
 12 aS1 casein gene
 16 <130> FILE REFERENCE: An127/Pri
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/524,295
 C--> 22 <141> CURRENT FILING DATE: 2005-02-11
 26 <150> PRIOR APPLICATION NUMBER: DE 102 38 433 A1
 28 <151> PRIOR FILING DATE: 2002-08-16
 32 <160> NUMBER OF SEQ ID NOS: 8
 36 <170> SOFTWARE: PatentIn version 3.1
 40 <210> SEQ ID NO: 1
 42 <211> LENGTH: 18
 44 <212> TYPE: DNA
 46 <213> ORGANISM: Bos spec.
 50 <220> FEATURE:
 W--> 52 <221> NAME/KEY: Primer 2
 54 <222> LOCATION: (1)..(18)
 56 <223> OTHER INFORMATION: 18 basepair, single stranded nucleic acid (linear)
 60 <400> SEQUENCE: 1
 61 gaagaagcag caagctgg 18
 64 <210> SEQ ID NO: 2
 66 <211> LENGTH: 19
 68 <212> TYPE: DNA
 70 <213> ORGANISM: Bos spec.
 74 <220> FEATURE:
 W--> 76 <221> NAME/KEY: Primer 3
 78 <222> LOCATION: (1)..(19)
 80 <223> OTHER INFORMATION: 19 basepair, single stranded nucleic acid (linear)
 84 <400> SEQUENCE: 2
 85 ccttgaata ttctaccag 19
 88 <210> SEQ ID NO: 3
 90 <211> LENGTH: 1061
 92 <212> TYPE: DNA
 94 <213> ORGANISM: Bos taurus
 98 <220> FEATURE:
 W--> 100 <221> NAME/KEY: alpha-S1Kaseingen
 102 <222> LOCATION: (1)..(1061)
 104 <223> OTHER INFORMATION: start Exon 1 at position 620
 108 <300> PUBLICATION INFORMATION:
 110 <301> AUTHORS: Koczan Dirk, Hobom Gerd, Seyfert Hans-Martin
 112 <302> TITLE: Genomic organization of the bovine alpha S1-casein gene
 114 <303> JOURNAL: Nucleic acids research

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116 <304> VOLUME: 19
 118 <305> ISSUE: 20
 120 <306> PAGES: 5591
 122 <307> DATE: 1991-09-24
 124 <308> DATABASE ACCESSION NO: X59856
 126 <309> DATABASE ENTRY DATE: 1991-07-18
 128 <313> RELEVANT RESIDUES: (1)..(1061)
 132 <300> PUBLICATION INFORMATION:
 134 <308> DATABASE ACCESSION NO: EMBL X59856
 136 <309> DATABASE ENTRY DATE: 1991-07-18
 138 <313> RELEVANT RESIDUES: (1)..(1061)
 142 <400> SEQUENCE: 3
 143 gaatgaatga actagttacc acaactagta caccaaaaat gaacaaaaaa tagcttggtg 60
 145 gtataattaa aatgccacca aaatttatac aataattata ttttctttt gcaggaaaaaa 120
 147 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg 180
 149 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt 240
 151 aataaaaattt gaaaaattttt gaagacccca ttttgcacca agaatttcat ttacaggtat 300
 153 tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa 360
 155 taaccataaa tctagggttt tggtgggtt ttttttgggtt tttttttttt tttttttttt 420
 157 attccatttc ctgtataatg agtcacttct ttgtgtaaa ctctccttag aatttcttgg 480
 159 gagaggaact gaacagaaca ttgatttctt atgtgagaga attcttagaa tttaaataaaa 540
 161 cctgttgggtt aaactgaaac cacaatattt gcattttact aatcagtagg tttaaataagc 600
 163 ttggaagcaa aagtctgcca tcaccccttcatcaacccca gcttgcgtct tcttccagt 660
 165 ctgggggttca aggtattatg tatacatata acaaaatttc tatgattttc ctctgtctca 720
 167 tcttcatttc ttcaactata cgcagttgtt actttctat gtgattgcaaa gtattggtagc 780
 169 ttccatgttataactgttta gcttaaaaat atattgcaaa atgttgcatac tatttatctc 840
 171 agagctataag gtgaaaaattt aaatactttt ataaagacca aattgatcat tttaaacgaa 900
 173 aattcttata tactgaaaat ttagatacat aacttcgtttagattttatgtt gtaaaataat 960
 175 ttgaatcattttgtcaat tctgtaaaaat gttgtcatac agaataattt ataaatatttt 1020
 177 ttttttcata gaaataaacat ttctggtaga atatttcaag g 1061
 180 <210> SEQ ID NO: 4
 182 <211> LENGTH: 652
 184 <212> TYPE: DNA
 186 <213> ORGANISM: Bos taurus
 190 <220> FEATURE:
 W--> 192 <221> NAME/KEY: CSN1S1-gene, 5`flanking region from position 616 and Exon 1 at position
 W--> 193 617
 195 <222> LOCATION: (1)..(652)
 197 <223> OTHER INFORMATION: Mutation/SNP position 83 (A to G), position 98 (A to G), position
 198 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1
 199 -bindingsite), position 541 (G to A);
 200 deletion TT between position 389 and 394 compared with Allel2
 204 <400> SEQUENCE: 4
 205 gaatgaatga actagttacc acaactagta caccaaaaat gaacaaaaaa tagcttggtg 60
 207 gtataattaa aatgccacca aagtttatac aataattgtt ttttctttt gcaggaaaaaa 120
 209 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg 180
 211 gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt 240
 213 aataaaaattt gaaaaattttt gaagacccca ttttgcacca agaatttctt ttacaggtat 300
 215 tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa 360

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217 taaccataaaa tctagggttt tggtgggtt ttttgggtt taattttagaa caatgccatt 420
 219 ccatttcctg tataatgagt cgcttccttg ttgtaaaactc tccttagaat ttcttggag 480
 221 aggaactgaa cagaacattt attcctatg tgagagaatt tttagaaattt aaataaaacct 540
 223 attggtaaaa ctgaaaccac aaaatttagca ttttactaat cagtaggtt aaatagctt 600
 225 gaagcaaaag tctgccccatca cttgtatcat caacccagct tgctgcttc tt 652
 228 <210> SEQ ID NO: 5
 230 <211> LENGTH: 654
 232 <212> TYPE: DNA
 234 <213> ORGANISM: Bos taurus
 238 <220> FEATURE:
 W--> 240 <221> NAME/KEY: CSN1S1-gene, 5`flanking region and Exon 1
 242 <222> LOCATION: (1)..(654)
 244 <223> OTHER INFORMATION: Bindingsite for transcriptionfactor AP-1 at position 438 to
 445
 245 Bindingsite for transcriptionfactor YY-1 at position 443 to 448
 249 <400> SEQUENCE: 5
 250 gaatgaatga actagttacc acaactagta caccaaaaat gaacaaaaaa tagttggtg 60
 252 gtataattaa aatgcacca aaatttatac aataattata ttttctttt gcaggaaaaa 120
 254 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg 180
 256 gattaactga gtttaaaag gtgaaataaa taatgaattc ttctcatgtt cttgtatgtt 240
 258 aataaaaattt gaaaaattttt gaagacccca ttttgcctca agaatttcat ttacaggtat 300
 260 tgaatttttca aaaggttaca aaggaaattt tattgtatata ataaatgcat gttctcataa 360
 262 taaccataaaa tctagggttt tggtgggtt tttttgttt gtttaatttag aacaatgcca 420
 264 ttccatttcc tgtataatga gtcacttctt tggtgaaac ttcctttaga atttcttggg 480
 266 agaggaactg aacagaacat tgatttccctt tggtgagagaa ttcttagaat taaataaaac 540
 268 ctgttggta aactgaaacc acaaaaattttag cattttacta atcagtaggtt taaatagct 600
 270 tggaaagcaaaa agtctgccccatca cttgtatcat atcaacccag ctgtctgtt tctt 654
 273 <210> SEQ ID NO: 6
 275 <211> LENGTH: 650
 277 <212> TYPE: DNA
 279 <213> ORGANISM: Bos taurus
 283 <220> FEATURE:
 W--> 285 <221> NAME/KEY: CSN1S1-gene, 5`flanking region
 287 <222> LOCATION: (1)..(650)
 289 <223> OTHER INFORMATION: Bindingsite for transcriptionfactor AP-1 at position 434 to
 441
 290 Bindingsite for transcriptionfactor YY-1 at position 439 to 444
 291 deletion G and TTT between 390 and 396 compaired with Allel 2
 295 <400> SEQUENCE: 6
 296 gaatgaatga actagttacc acaactagta caccaaaaat gaacaaaaaa tagttggtg 60
 298 gtataattaa aatgcacca aaatttatac aataattata ttttctttt gcaggaaaaa 120
 300 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg 180
 302 gattaactga gtttaaaag gtgaaataaa taatgaattc ttctcatgtt cttgtatgtt 240
 304 aataaaaattt gaaaaattttt gaagacccca ttttgcctca agaatttcat ttacaggtat 300
 306 tgaatttttca aaaggttaca aaggaaattt tattgtatata ataaatgcat gttctcataa 360
 308 taaccataaaa tctagggttt tggtgggtt tttttgtta attttagaaca atgcccattcc 420
 310 atttcctgtt taatgagtca cttctttgtt gtaaactctc ctttagaaattt cttggagag 480
 312 gaactgaaca gaacattgtt ttcctatgtt agagaattct tagaatttaa ataaacctgt 540
 314 tggttaaactt gaaaccacaa aatttagcatt ttactaatca gtaggtttaa atagcttgg 600
 316 agcaaaaatgtc tgccatcacc ttgtatcatca acccagctt ctgtcttctt 650
 319 <210> SEQ ID NO: 7

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321 <211> LENGTH: 650
 323 <212> TYPE: DNA
 325 <213> ORGANISM: Bos taurus
 329 <220> FEATURE:
 W--> 331 <221> NAME/KEY: CSN1S1-gene, 5`flanking region
 333 <222> LOCATION: (1)..(650)
 335 <223> OTHER INFORMATION: Bindingsite for transcriptionfactors: AP-1 at position 434
 to 441
 336 , ABF1 at position 469 to 483, YY-1 at position 439 to 444;
 337 mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
 338 gsite;
 W--> 339 deletion G and TTT between position 390 and 396 compaired with A1
 W--> 340 lel 2
 344 <400> SEQUENCE: 7
 345 gaatgaatga actagttacc acaactagta caccaaaaat gaacaaaaaa tagcttggtg 60
 347 gtataattaa aatgccacca aaatttatac aataattata ttttctttt gcaggaaaaa 120
 349 gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg 180
 351 gattaactga gtttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt 240
 353 aataaaaattt gaaaaattttt gaagacccca ttttgcacca agaatttcat ttacaggtat 300
 355 tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa 360
 357 taaccataaa tctagggttt tggtggggtt tttttgtta atttagaaca atgccattcc 420
 359 attcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagac 480
 361 gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt 540
 363 tggtaaact gaaaccacaa aattagcatt ttactaatca gtaggttaa atagcttgg 600
 365 agcaaaagtc tgccatcacc ttgatcatca acccagctt ctgctttctt 650
 368 <210> SEQ ID NO: 8
 370 <211> LENGTH: 20
 372 <212> TYPE: DNA
 374 <213> ORGANISM: Bos spec.
 378 <220> FEATURE:
 W--> 380 <221> NAME/KEY: Primer1
 382 <222> LOCATION: (1)..(20)
 384 <223> OTHER INFORMATION: 20 basepair, single stranded nucleic acid (linear)
 388 <400> SEQUENCE: 8
 389 gaatgaatga actagttacc 20

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/524,295

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Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\01052006\J524295.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application Number
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:52 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:76 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:193 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:240 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:285 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:331 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:339 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:340 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:380 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8